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REMARKS

In the official communication dated June 28, 2001, the Examiner states that Applicants' Amendment filed May 7, 2001 is not fully responsive to the Office Action mailed November 3, 2000. Specifically, the Examiner points out that the sequences at page 20, lines 11, 12 and 14, and the sequences in Table 7 do not comply with the sequence rules under 37 C.F.R. §§1.821-1.825.

In response, Applicants are providing herewith a substitute paper and computer-readable copy of the Sequence Listing, together with a statement under 37 C.F.R. §1.821(f) verifying that the content of the paper and the computer copy of the Sequence Listing are the same and that no new matter is introduced. A copy of the notice is also enclosed.

Applicants submit that the substitute Sequence Listing includes the sequences disclosed at page 20, lines 11, 12 and 14 as SEQ ID NO: 43, SEQ ID NO: 44 and SEQ ID NO: 45, respectively. The specification has also been amended at page 20, lines 11, 12 and 14 to insert these sequence identifiers.

Applicants further submit that the substitute Sequence Listing also includes the sequences disclosed in Table 7. More specifically, the sequences designated as sequence A, B, C, D, E, F, G, H, I, J and K, are listed as SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 42, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25 and SEQ ID NO: 41, respectively. The specification has been amended to insert these sequence identifiers at page 91, lines 9-11. Applicants respectfully point out to the Examiner that the sequence designated as Sequence K in Table 7 was listed as SEQ ID NO: 27 in the Sequence Listing previously submitted, and is now listed as SEQ ID NO: 41 in the substitute Sequence Listing submitted herewith. Applicants have also renumbered the sequence identifiers of SEQ ID NO: 28 through SEQ ID NO: 41 in the prior listing to SEQ ID NO: 27 through SEQ ID NO: 40. It is respectfully submitted that this amendment to the assignment of sequence

identifiers does not introduce new matter. Support for this amendment is found throughout the specification, particularly, in Table 3 at pages 29-30.

By way of the substitute Sequence Listing, Applicants have also corrected two clerical errors in SEQ ID NO: 3 and SEQ ID NO: 4 in the prior listing. The errors and the correction are indicated in the attached marked-up copy of the Sequence Listing. Support for the sequence of SEQ ID NO: 4 is found in Table 7, Sequence B, at pages 93-97, and in Table 3 at page 29 of the specification. The errors in SEQ ID NO: 3, which encodes the protein sequence of SEQ ID NO: 4, have also been corrected.

Furthermore, Applicants have amended the information in the field <223> for SEQ ID NO: 30, 32 and 35 (SEQ ID NO: 31, 33 and 36 in the prior listing). Specifically, the sequences of SEQ ID NO: 30, 32 and 35 are not "oligonucleotides" as indicated in the prior Sequence Listing, but are "synthetic peptides representing a conserved region in plant cytochrome p450 sequences", as described at page 29, line 26 to page 30, line 11 of the specification.

Applicants respectfully submit that the specification has been amended at page 20 and 91 to insert the sequence identifiers, as discussed above. The specification has also been amended at page 55, line 6, by replacing the petal colour designation for the Skr4 x Sw63 control "(RHSCC# 74C)" with "(RHSCC# 75C)". Support for this amendment can be found throughout the specification and in particular at page 67, line 9 and at page 80, line 21. In addition, the specification has been amended at 79, line 14-15, by deleting the reference to the snapdragon sdF3'H clone as "(SEQ ID NO:3 and SEQ ID NO:4)" and inserting therefor "(SEQ ID NO:5 and SEQ ID NO:6)". Support for this amendment can be found in Table 3 at page 29 of the specification.

It is respectfully submitted that the foregoing amendment to the Sequence Listing and the specification does not introduce new matter. Attached hereto is a marked-up version of the changes made to the specification and the Sequence Listing by the current amendment, which is captioned **"Version with markings to show changes made."**

In view of the foregoing amendments and remarks, it is firmly believed that the subject application is in condition for allowance, which action is earnestly solicited.

Respectfully submitted,

A handwritten signature in black ink, appearing to read 'P. I. Bernstein', with a long horizontal flourish extending to the right.

Peter I. Bernstein
Registration Number 43,497

Scully, Scott, Murphy & Presser
400 Garden City Plaza
Garden City, New York 11530
Telephone: 516-742-4343

PIB/XZ:ab

Encls.: Version with Markings to Show Changes Made (including marked up copy of the amended pages of the sequence listing);
Substitute paper copy of the sequence listing;
Substitute computer readable copy of the sequence listing;
Copy of Notice to Comply; and
Statement Under 37 C.F.R. §1.821(f)

Appln. No.: 09/142,108
Date: August 28, 2001

Version With Markings to Show Changes Made

In the Specification:

Please amend the paragraph beginning at page 20, line 8 as follows:

Another aspect of the present invention provides a nucleic acid molecule comprising a sequence of nucleotides encoding or complementary to a sequence of nucleotides encoding a F3'H, wherein the translation of the said nucleic acid molecule comprises the amino acid sequence RPPNSGA (SEQ ID NO:43). Preferably, the translation of the said nucleic acid molecule comprises the amino acid sequence RPPNSGAXHXAYNYXDL (SEQ ID NO:44) and still more preferably the translation of the said nucleic acid molecule comprises the amino acid sequence RPPNSGAXHXAYNYXDL[X]_nGGEK (SEQ ID NO:45), where X represents any amino acid and [X]_n represents an amino acid sequence of from 0 to 500 amino acids.

Please amend the paragraph beginning at page 55, line 3 as follows:

The expression of the introduced KC-1 cDNA in the Skr4 x SW63 hybrid had a marked effect on flower colour. Ten of the twelve transgenic plants transformed with pCGP1810 produced flowers with an altered petal colour (RHSCC# 73A), compared with the Skr4 x Sw63 control (RHSCC# [74]75C). Moreover the anthers and pollen of the transgenic flowers were pink, compared with those of the control Skr4 x SW63 plant, which were white.[.] In addition, expression of the KC-1 cDNA in the Skr4 x SW63 hybrid conferred a dark pink hue to the corolla, which is normally pale lilac. The colour codes are taken from the Royal Horticultural Society's Colour Chart (RHSCC). They provide an alternative means by which to

describe the colour phenotypes observed. The designated numbers, however, should be taken only as a guide to the perceived colours and should not be regarded as limiting the possible colours which may be obtained.

Please amend the paragraph beginning at page 79, line 12 as follows:

The nucleotide and predicted amino acid sequences of the rose F3'H #34 cDNA clone (SEQ ID NO:14 and SEQ ID NO:15) were compared with those of the petunia OGR-38 F3'H cDNA clone (SEQ ID NO:1 and SEQ ID NO:2) and the snapdragon sd F3'H clone [(SEQ ID NO:3 and SEQ ID NO:4)] (SEQ ID NO:5 and SEQ ID NO:6). The rose F3'H #34 cDNA clone showed 64.7% similarity, over 1651 nucleotides and 72.7% similarity, over 509 amino acids, to that of the petunia OGR-38 cDNA clone, and 67.2% similarity, over 1507 nucleotides, and 68.9 similarity, over 502 amino acids, to that of the snapdragon sdF3'H clone.

Please amend the paragraph beginning at page 91, line 7 as follows:

Multiple sequence alignments were performed using the ClustalW program as described in Example 3. Table 7 (below) provides a multiple sequence alignment of the predicted amino acid sequences of petunia OGR-38 (A) (SEQ ID NO:2); carnation (B) (SEQ ID NO:4); snapdragon (C) (SEQ ID NO:6); arabidopsis Tt7 coding region (D) (SEQ ID NO:42); rose (E) (SEQ ID NO:15) chrysanthemum (F) (SEQ ID NO:17); torenia (G) (SEQ ID NO:19); morning glory (H) (SEQ ID NO:21); gentian (partial sequence) (I) (SEQ ID NO:23); lisianthus (partial sequence) (J) (SEQ ID NO:25) and the petunia 651 cDNA (K) (SEQ ID NO:41). Conserved amino acids are shown in bolded capital letters and are boxed and shaded. Similar amino acids are shown in capital letters and are only lightly shaded, and dissimilar amino acids are shown in lower case letters.

In the Sequence Listing:

The Sequence Listing has been amended at page 1, and in SEQ ID NO: 3 (pages 5-8), SEQ ID NO: 4 (pages 8-9), and SEQ ID NO: 27 through SEQ ID NO: 41, as follows (beginning at the next page). SEQ ID NO: 42 to SEQ ID NO: 45 have been added.



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Applicati n No.: 09/142,108

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☒ 7. Other: Sequences at page 20 in Table 7 are missing from the Sequence Listing

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

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MARKED UP COPY OF SEQUENCE LISTING
SEQUENCE LISTING

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and uses therefor
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<160> ~~41~~ 45

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Leu Ser Leu Ile Leu Tyr Thr Val Ile Phe Ser Phe Leu Leu Gln Phe
5 10 15

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Ile Leu Arg Ser Phe Phe Arg Lys Arg Tyr Pro Leu Pro Leu Pro Pro
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Gly Pro Lys Pro Trp Pro Ile Ile Gly Asn Leu Val His Leu Gly Pro
40 45 50

aaa cca cat caa tca act gca gcc atg gct caa act tat gga cca ctc 250
Lys Pro His Gln Ser Thr Ala Ala Met Ala Gln Thr Tyr Gly Pro Leu

-----55-----60-----65-----
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| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Ile | Pro | Gln | Leu | Asn | Trp | Leu | Asp | Ile | Gln | Gly | Val | Ala | Ala | Lys | 225 | 230 | 235 | 240 |
| Met | Lys | Lys | Leu | His | Ala | Arg | Phe | Asp | Ala | Phe | Leu | Thr | Asp | Ile | Leu | 245 | 250 | | 255 |
| Glu | Glu | His | Lys | Gly | Lys | Ile | Phe | Gly | Glu | Met | Lys | Asp | Leu | Leu | Ser | 260 | 265 | | 270 |
| Thr | Leu | Ile | Ser | Leu | Lys | Asn | Asp | Asp | Ala | Asp | Asn | Asp | Gly | Gly | Lys | 275 | 280 | | 285 |
| Leu | Thr | Asp | Thr | Glu | Ile | Lys | Ala | Leu | Leu | Leu | Asn | Leu | Phe | Val | Ala | 290 | 295 | 300 | |
| Gly | Thr | Asp | Thr | Ser | Ser | Ser | Thr | Val | Glu | Trp | Ala | Ile | Ala | Glu | Leu | 305 | 310 | 315 | 320 |
| Ile | Arg | Asn | Pro | Lys | Ile | Leu | Ala | Gln | Ala | Gln | Gln | Glu | Ile | Asp | Lys | 325 | 330 | | 335 |
| Val | Val | Gly | Arg | Asp | Arg | Leu | Val | Gly | Glu | Leu | Asp | Leu | Ala | Gln | Leu | 340 | 345 | | 350 |
| Thr | Tyr | Leu | Glu | Ala | Ile | Val | Lys | Glu | Thr | Phe | Arg | Leu | His | Pro | Ser | 355 | 360 | | 365 |
| Thr | Pro | Leu | Ser | Leu | Pro | Arg | Ile | Ala | Ser | Glu | Ser | Cys | Glu | Ile | Asn | 370 | 375 | 380 | |
| Gly | Tyr | Phe | Ile | Pro | Lys | Gly | Ser | Thr | Leu | Leu | Leu | Asn | Val | Trp | Ala | 385 | 390 | 395 | 400 |
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| Glu | Arg | Phe | Leu | Pro | Gly | Gly | Glu | Lys | Pro | Lys | Val | Asp | Val | Arg | Gly | 420 | 425 | | 430 |
| Asn | Asp | Phe | Glu | Val | Ile | Pro | Phe | Gly | Ala | Gly | Arg | Arg | Ile | Cys | Ala | 435 | 440 | | 445 |
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| Ile | His | Ala | Phe | Asn | Trp | Asp | Leu | Val | Ser | Gly | Gln | Leu | Pro | Glu | Met | 465 | 470 | 475 | 480 |
| Leu | Asn | Met | Glu | Glu | Ala | Tyr | Gly | Leu | Thr | Leu | Gln | Arg | Ala | Asp | Pro | 485 | 490 | | 495 |
| Leu | Val | Val | His | Pro | Arg | Pro | Arg | Leu | Glu | Ala | Gln | Ala | Tyr | Ile | Gly | 500 | 505 | | 510 |

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aaaaaaaaatt ataatgtcac ccttagaggt aactttctac accatagtcc t atg cac 177
Met His
1

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Asn Leu Tyr Tyr Leu Ile Thr Thr Val Phe Arg Gly His Gln Lys Pro
5 10 15

ctt cct cca ggg cca cga cca tgg ccc atc gtg gga aac ctc cca cat 273
Leu Pro Pro Gly Pro Arg Pro Trp Pro Ile Val Gly Asn Leu Pro His
20 25 30

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Met Gly Gln Ala Pro His Gln Gly Leu Ala Ala Leu Ala Gln Lys Tyr
35 40 45 50

ggc cct cta ttg tat atg aga ctg ggg tac gtg gac gtt gtt gtg gcc 369
Gly Pro Leu Leu Tyr Met Arg Leu Gly Tyr Val Asp Val Val Val Ala
55 60 65

gcc tca gcg tct gta gcg acc cag ttt ctt aag aca cat gac cta aat 417
Ala Ser Ala Ser Val Ala Thr Gln Phe Leu Lys Thr His Asp Leu Asn
70 75 80

ttt tcg agt agg cca ccg aat tcg ggg gct aaa cac att gct tat aac 465
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85 90 95

tat caa gac ctt gtt ttt gca cct tat gga cct aaa tgg cgc atg ctt 513
Tyr Gln Asp Leu Val Phe Ala Pro Tyr Gly Pro Lys Trp Arg Met Leu
100 105 110

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Arg Lys Ile Cys Ser Leu His Met Phe Ser Ser Lys Ala Leu Asp Asp
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ttt aga ctt gtc cgt cag gaa gaa gta tct ata ctg gta aat gcg ata 609
Phe Arg Leu Val Arg Gln Glu Glu Val Ser Ile Leu Val Asn Ala Ile
135 140 145

gca aaa gca gga aca aag cca gta caa cta gga caa cta ctc aac gtg 657
Ala Lys Ala Gly Thr Lys Pro Val Gln Leu Gly Gln Leu Leu Asn Val
150 155 160

tgc acc aca aat gcc tta tcg agg gtg atg cta ggg aag cga gtt ctc 705
Cys Thr Thr Asn Ala Leu Ser Arg Val Met Leu Gly Lys Arg Val Leu
165 170 175

ggg gat ggc aca ggg aaa agc gac cca aaa gcc gag gaa ttt aag gac 753

| | | | | | | | | | | | | | | | | | |
|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|------|--|
| Gly | Asp | Gly | Thr | Gly | Lys | Ser | Asp | Pro | Lys | Ala | Glu | Glu | Phe | Lys | Asp | | |
| 180 | | | | | | 185 | | | | | 190 | | | | | | |
| atg | gtg | ctg | gag | tta | atg | ggt | ctc | acc | gga | ggt | ttt | aac | att | ggc | gat | 801 | |
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| 195 | | | | | 200 | | | | 205 | | | | | | 210 | | |
| ttt | gta | ccg | gca | ttg | gaa | tgt | cta | gac | tta | caa | ggg | ggt | gca | tct | aaa | 849 | |
| Phe | Val | Pro | Ala | Leu | Glu | Cys | Leu | Asp | Leu | Gln | Gly | Val | Ala | Ser | Lys | | |
| | | | | 215 | | | | | 220 | | | | | 225 | | | |
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| Met | Lys | Lys | Leu | His | Lys | Arg | Leu | Asp | Asn | Phe | Met | Ser | Asn | Ile | Leu | | |
| | | | 230 | | | | | 235 | | | | | 240 | | | | |
| gag | gaa | cac | aag | agt | ggt | gca | cat | caa | caa | aat | ggg | gga | gat | ttg | cta | 945 | |
| Glu | Glu | His | Lys | Ser | Val | Ala | His | Gln | Gln | Asn | Gly | Gly | Asp | Leu | Leu | | |
| | | 245 | | | | | 250 | | | | | 255 | | | | | |
| agc | att | ttg | ata | tct | ttg | aag | gat | aat | tgt | gat | ggg | gaa | ggg | ggc | aag | 993 | |
| Ser | Ile | Leu | Ile | Ser | Leu | Lys | Asp | Asn | Cys | Asp | Gly | Glu | Gly | Gly | Lys | | |
| | 260 | | | | | 265 | | | | | 270 | | | | | | |
| ttt | agt | gcc | aca | gaa | att | aag | gcc | ttg | cta | ttg | gat | tta | ttt | aca | gct | 1041 | |
| Phe | Ser | Ala | Thr | Glu | Ile | Lys | Ala | Leu | Leu | Leu | Asp | Leu | Phe | Thr | Ala | | |
| 275 | | | | | 280 | | | | | 285 | | | | | 290 | | |
| gga | aca | gac | aca | tca | tct | agt | aca | act | gaa | tgg | gcc | ata | gcc | gaa | cta | 1089 | |
| Gly | Thr | Asp | Thr | Ser | Ser | Ser | Thr | Thr | Glu | Trp | Ala | Ile | Ala | Glu | Leu | | |
| | | | | 295 | | | | | 300 | | | | | 305 | | | |
| att | cgc | cat | cca | aaa | atc | tta | gcc | caa | ggt | caa | caa | gaa | atg | gac | tca | 1137 | |
| Ile | Arg | His | Pro | Lys | Ile | Leu | Ala | Gln | Val | Gln | Gln | Glu | Met | Asp | Ser | | |
| | | | 310 | | | | | 315 | | | | | 320 | | | | |
| gtc | gtg | ggc | cga | gac | cga | ctc | ata | gcc | gaa | gct | gac | ata | ccg | aac | cta | 1185 | |
| Val | Val | Gly | Arg | Asp | Arg | Leu | Ile | Ala | Glu | Ala | Asp | Ile | Pro | Asn | Leu | | |
| | | 325 | | | | | 330 | | | | | 335 | | | | | |
| acc | tac | ttc | caa | gcc | gta | atc | aaa | gag | ggt | ttc | cga | ctt | cac | ccg | tcc | 1233 | |
| Thr | Tyr | Phe | Gln | Ala | Val | Ile | Lys | Glu | Val | Phe | Arg | Leu | His | Pro | Ser | | |
| | 340 | | | | | 345 | | | | 350 | | | | | | | |
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| Gly | Tyr | His | Ile | Pro | Lys | Asn | Thr | Thr | Leu | Leu | Val | Asn | Val | Trp | Ala | | |
| | | | | 375 | | | | | 380 | | | | | 385 | | | |
| atc | gca | cgc | gac | cct | gag | ggt | tgg | gcc | gac | ccg | tta | gag | ttt | aaa | ccc | 1377 | |

Ile Ala Arg Asp Pro Glu Val Trp Ala Asp Pro Leu Glu Phe Lys Pro
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35 40 45
Lys Tyr Gly Pro Leu Leu Tyr Met Arg Leu Gly Tyr Val Asp Val Val
50 55 60
Val Ala Ala Ser Ala Ser Val Ala Thr Gln Phe Leu Lys Thr His Asp
65 70 75 80
Leu Asn Phe Ser Ser Arg Pro Pro Asn Ser Gly Ala Lys His Ile Ala
85 90 95
Tyr Asn Tyr Gln Asp Leu Val Phe Ala Pro Tyr Gly Pro Lys Trp Arg
100 105 110

| | | | | | | | | | | | | | | | |
|-------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
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| | 115 | | | | | | 120 | | | | | 125 | | | |
| Asp | Asp | Phe | Arg | Leu | Val | Arg | Gln | Glu | Glu | Val | Ser | Ile | Leu | Val | Asn |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Ala | Ile | Ala | Lys | Ala | Gly | Thr | Lys | Pro | Val | Gln | Leu | Gly | Gln | Leu | Leu |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Asn | Val | Cys | Thr | Thr | Asn | Ala | Leu | Ser | Arg | Val | Met | Leu | Gly | Lys | Arg |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Val | Leu | Gly | Asp | Gly | Thr | Gly | Lys | Ser | Asp | Pro | Lys | Ala | Glu | Glu | Phe |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Lys | Asp | Met | Val | Leu | Glu | Leu | Met | Val | Leu | Thr | Gly | Val | Phe | Asn | Ile |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Gly | Asp | Phe | Val | Pro | Ala | Leu | Glu | Cys | Leu | Asp | Leu | Gln | Gly | Val | Ala |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Ser | Lys | Met | Lys | Lys | Leu | His | Lys | Arg | Leu | Asp | Asn | Phe | Met | Ser | Asn |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Ile | Leu | Glu | Glu | His | Lys | Ser | Val | Ala | His | Gln | Gln | Asn | Gly | Gly | Asp |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Leu | Leu | Ser | Ile | Leu | Ile | Ser | Leu | Lys | Asp | Asn | Cys | Asp | Gly | Glu | Gly |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Gly | Lys | Phe | Ser | Ala | Thr | Glu | Ile | Lys | Ala | Leu | Leu | Leu | Asp | Leu | Phe |
| | | 275 | | | | | 280 | | | | | 285 | | | |
| Thr | Ala | Gly | Thr | Asp | Thr | Ser | Ser | Ser | Thr | Thr | Glu | Trp | Ala | Ile | Ala |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Glu | Leu | Ile | Arg | His | Pro | Lys | Ile | Leu | Ala | Gln | Val | Gln | Gln | Glu | Met |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| Asp | Ser | Val | Val | Gly | Arg | Asp | Arg | Leu | Ile | Ala | Glu | Ala | Asp | Ile | Pro |
| | | | | 325 | | | | | 330 | | | | | 335 | |
| Asn | Leu | Thr | Tyr | Phe | Gln | Ala | Val | Ile | Lys | Glu | Val | Phe | Arg | Leu | His |
| | | | 340 | | | | | 345 | | | | | 350 | | |
| Pro | Ser | Thr | Pro | Leu | Ser | Leu | Pro | Arg | Val | Ala | Asn | Glu | Ser | Cys | Glu |
| | | 355 | | | | | 360 | | | | | 365 | | | |
| Ile | Asn | Gly | Tyr | His | Ile | Pro | Lys | Asn | Thr | Thr | Leu | Leu | Val | Asn | Val |
| | 370 | | | | | 375 | | | | | 380 | | | | |
| Trp | Ala | Ile | Ala | Arg | Asp | Pro | Glu | Val | Trp | Ala | Asp | Pro | Leu | Glu | Phe |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 |
| Lys | Pro | Glu | Arg | Phe | Leu | Pro | Gly | Gly | Glu | Lys | Pro | Asn | Val | Asp | Val |
| | | | | 405 | | | | | 410 | | | | | 415 | |
| Lys | Gly | Asn | Asp | Phe | Glu | Leu | Ile | Pro | Phe | Gly | Ala | Gly | Arg | Arg | Ile |
| | | | 420 | | | | | 425 | | | | | 430 | | |
| Cys | Ala | Gly | Leu | Ser | Leu | Gly | Leu | Arg | Met | Val | Gln | Leu | Met | Thr | Ala |
| | | 435 | | | | | 440 | | | | | 445 | | | |
| Thr | Leu | Ala | His | Thr | Tyr | Asp | Trp | Ala | Leu | Ala | Asp | Gly | Leu | Met | Pro |
| | | | | | | 455 | | | | | 460 | | | | |
| Glu</ | | | | | | | | | | | | | | | |

gaggttttaa gttactagta gattctattg cagctatagg atttctttca ccatcacgta 1605
 tgctttaccg ttggatgatg gaaagaaata tctatagctt tgggtttggt tagtttgcac 1665
 ataaaaattg aatgaatgga ataccatgga gttataagaa ataataagac tatgattctt 1725
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<210> *21 41 (forty-one)*

<211> 496

<212> PRT

<213> Petunia sp.

<400> *21 41*

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| Met | Asp | Tyr | Val | Asn | Ile | Leu | Leu | Gly | Leu | Phe | Phe | Thr | Trp | Phe | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Val | Asn | Gly | Leu | Met | Ser | Leu | Arg | Arg | Arg | Lys | Ile | Ser | Lys | Lys | Leu |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Pro | Pro | Gly | Pro | Phe | Pro | Leu | Pro | Ile | Ile | Gly | Asn | Leu | His | Leu | Leu |
| | | | 35 | | | | 40 | | | | | 45 | | | |
| Gly | Asn | His | Pro | His | Lys | Ser | Leu | Ala | Gln | Leu | Ala | Lys | Ile | His | Gly |
| | 50 | | | | | 55 | | | | 60 | | | | | |
| Pro | Ile | Met | Asn | Leu | Lys | Leu | Gly | Gln | Leu | Asn | Thr | Val | Val | Ile | Ser |
| 65 | | | | | 70 | | | | 75 | | | | | 80 | |
| Ser | Ser | Val | Val | Ala | Arg | Glu | Val | Leu | Gln | Lys | Gln | Asp | Leu | Thr | Phe |
| | | | | 85 | | | | 90 | | | | | 95 | | |
| Ser | Asn | Arg | Phe | Val | Pro | Asp | Val | Val | His | Val | Arg | Asn | His | Ser | Asp |
| | | | 100 | | | | 105 | | | | | 110 | | | |
| Phe | Ser | Val | Val | Trp | Leu | Pro | Val | Asn | Ser | Arg | Trp | Lys | Thr | Leu | Arg |
| | 115 | | | | | 120 | | | | | 125 | | | | |
| Lys | Ile | Met | Asn | Ser | Ser | Ile | Phe | Ser | Gly | Asn | Lys | Leu | Asp | Gly | Asn |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Gln | His | Leu | Arg | Ser | Lys | Lys | Val | Gln | Glu | Leu | Ile | Asp | Tyr | Cys | Gln |
| 145 | | | | | 150 | | | | 155 | | | | | 160 | |
| Lys | Cys | Ala | Lys | Asn | Gly | Glu | Ala | Val | Asp | Ile | Gly | Arg | Ala | Thr | Phe |
| | | | 165 | | | | | 170 | | | | | 175 | | |
| Gly | Thr | Thr | Leu | Asn | Leu | Leu | Ser | Asn | Thr | Ile | Phe | Ser | Lys | Asp | Leu |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Thr | Asn | Pro | Phe | Ser | Asp | Ser | Ala | Lys | Glu | Phe | Lys | Glu | Leu | Val | Trp |
| | 195 | | | | | 200 | | | | | 205 | | | | |
| Asn | Ile | Met | Val | Glu | Ala | Gly | Lys | Pro | Asn | Leu | Val | Asp | Tyr | Phe | Pro |
| | 210 | | | | 215 | | | | | 220 | | | | | |
| Phe | Leu | Glu | Lys | Ile | Asp | Pro | Gln | Gly | Ile | Lys | Arg | Arg | Met | Thr | Asn |
| 225 | | | | 230 | | | | | 235 | | | | | 240 | |
| Asn | Phe | Thr | Lys | Phe | Leu | Gly | Leu | Ile | Ser | Gly | Leu | Ile | Asp | Asp | Arg |
| | | | 245 | | | | | 250 | | | | | 255 | | |
| Leu | Lys | Glu | Arg | Asn | Leu | Arg | Asp | Asn | Ala | Asn | Ile | Asp | Val | Leu | Asp |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Ala | Leu | Leu | Asn | Ile | Ser | Gln | Glu | Asn | Pro | Glu | Glu | Ile | Asp | Arg | Asn |
| | 275 | | | | | 280 | | | | | | 285 | | | |
| Gln | Ile | Glu | Gln | Leu | Cys | Leu | Asp | Leu | Phe | Ala | Ala | Gly | Thr | Asp | Thr |

| | | | | |
|---|-----|-----|-----|-----|
| 290 | | 295 | | 300 |
| Thr Ser Asn Thr Leu Glu Trp Ala Met Ala Glu Leu Leu Gln Asn Pro | | | | |
| 305 | | 310 | | 315 |
| His Thr Leu Gln Lys Ala Gln Glu Glu Leu Ala Gln Val Ile Gly Lys | | | | |
| | 325 | | 330 | 335 |
| Gly Lys Gln Val Glu Glu Ala Asp Val Gly Arg Leu Pro Tyr Leu Arg | | | | |
| | 340 | | 345 | 350 |
| Cys Ile Val Lys Glu Thr Leu Arg Ile His Pro Ala Ala Pro Leu Leu | | | | |
| | 355 | | 360 | 365 |
| Ile Pro Arg Lys Val Glu Glu Asp Val Glu Leu Ser Thr Tyr Ile Ile | | | | |
| | 370 | | 375 | 380 |
| Pro Lys Asp Ser Gln Val Leu Val Asn Val Trp Ala Ile Gly Arg Asn | | | | |
| 385 | | 390 | | 395 |
| Ser Asp Leu Trp Glu Asn Pro Leu Val Phe Lys Pro Glu Arg Phe Trp | | | | |
| | 405 | | 410 | 415 |
| Glu Ser Glu Ile Asp Ile Arg Gly Arg Asp Phe Glu Leu Ile Pro Phe | | | | |
| | 420 | | 425 | 430 |
| Gly Ala Gly Arg Arg Ile Cys Pro Gly Leu Pro Leu Ala Met Arg Met | | | | |
| | 435 | | 440 | 445 |
| Ile Pro Val Ala Leu Gly Ser Leu Leu Asn Ser Phe Asn Trp Lys Leu | | | | |
| | 450 | | 455 | 460 |
| Tyr Gly Gly Ile Ala Pro Lys Asp Leu Asp Met Gln Glu Lys Phe Gly | | | | |
| 465 | | 470 | | 475 |
| Ile Thr Leu Ala Lys Ala Gln Pro Leu Leu Ala Ile Pro Thr Pro Leu | | | | |
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<210> ~~26~~ 27

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:oligonucleotide

<400> ~~26~~ 27

tttttttttt ttttttta

18

<210> ~~26~~ 28

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:oligonucleotide

<400> ~~26~~ 28

tttttttttt tttttttc

18

<210> ~~30~~ 29

<211> 18
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:oligonucleotide

<400> ~~30~~ 29
tttttttttt tttttttg

18

<210> ~~30~~ 30
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:oligonucleotide

<400> ~~30~~ 30
Trp Ala Ile Gly Arg Asp Pro
1 5

*Synthetic peptide
representing a conserved
amino acid region in
plant cytochrome P450 sequences.*

<210> ~~30~~ 31
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:oligonucleotide

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<222> (6)
<223> n is inosine

<220>
<221> Modified Base
<222> (9)
<223> n is inosine

<220>
<221> Modified Base
<222> (12)
<223> n is inosine

<220>
<221> Modified Base
<222> (15)
<223> n is inosine

<400> ~~30~~ 31

tgggcnatng gnmngaycc

20

<210> ~~32~~ 32

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: ~~primer~~ *Synthetic peptide representing a conserved region in plant cytochrome p450 sequences.*

<400> ~~32~~ 32

Phe Arg Pro Glu Arg Phe

1

5

<210> ~~33~~ 33

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: oligonucleotide

<220>

<221> Modified base

<222> (11)

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<220>

<221> Modified base

<222> (14)

<223> n is inosine

<220>

<221> Modified base

<222> (20)

<223> n is inosine

<400> ~~33~~ 33

aggaattymg nccngarmgn tt

22

<210> ~~34~~ 34

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: oligonucleotide

<220>

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<222> (3)
<223> n is inosine

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<400> ~~36~~ 34
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32

<210> ~~36~~ 35
<211> 7
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<220>
<223> Description of Artificial Sequence: oligonucleotide

<400> ~~36~~ 35
Glu Phe Xaa Pro Glu Arg Phe
1 5

Synthetic peptide representing a
conserved region in
plant cytochrome P450
sequences.

<210> ~~31~~ 36
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide

<220>
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<223> n is inosine

<220>
<221> Modified base
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<223> n is inosine

<220>
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<222> (9)
<223> n is inosine

<220>
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<222> (12)
<223> n is inosine

<220>
<221> Modified base
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<223> n is inosine

<220>
<221> Modified base
<222> (18)
<223> n is inosine

<400> ~~31~~ 36
ganttynnnc cnganmgntt

20

<210> ~~36~~ 37
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide

<400> ~~36~~ 37
 ccacacgagt agttttggca ttgaccc 28

<210> ~~36~~ 38
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:oligonucleotide

<400> ~~36~~ 38
 gtcttggaca tcacacttca atctg 25

<210> ~~36~~ 39
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 <212> DNA
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<220>
 <223> Description of Artificial Sequence:oligonucleotide

<400> ~~40~~ 39
 ccgaattccc cccccc 17

<210> ~~41~~ 40
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<220>
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<400> ~~41~~⁴⁰
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32

<210> 41 (previous SEQ ID NO: 27).

Please also del SEQ ID NO: 42-45 as indicated beginning from next page.

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Pro | Gly | Pro | Phe | Pro | Leu | Pro | Ile | Ile | Gly | Asn | Leu | His | Leu | Leu |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Gly | Asn | His | Pro | His | Lys | Ser | Leu | Ala | Gln | Leu | Ala | Lys | Ile | His | Gly |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Pro | Ile | Met | Asn | Leu | Lys | Leu | Gly | Gln | Leu | Asn | Thr | Val | Val | Ile | Ser |
| | 65 | | | | 70 | | | | | 75 | | | | | 80 |
| Ser | Ser | Val | Val | Ala | Arg | Glu | Val | Leu | Gln | Lys | Gln | Asp | Leu | Thr | Phe |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Ser | Asn | Arg | Phe | Val | Pro | Asp | Val | Val | His | Val | Arg | Asn | His | Ser | Asp |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Phe | Ser | Val | Val | Trp | Leu | Pro | Val | Asn | Ser | Arg | Trp | Lys | Thr | Leu | Arg |
| | | 115 | | | | 120 | | | | | | 125 | | | |
| Lys | Ile | Met | Asn | Ser | Ser | Ile | Phe | Ser | Gly | Asn | Lys | Leu | Asp | Gly | Asn |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| | | | | | | | | | | | | | | | |
| Gln | His | Leu | Arg | Ser | Lys | Lys | Val | Gln | Glu | Leu | Ile | Asp | Tyr | Cys | Gln |
| | 145 | | | | 150 | | | | | 155 | | | | | 160 |
| Lys | Cys | Ala | Lys | Asn | Gly | Glu | Ala | Val | Asp | Ile | Gly | Arg | Ala | Thr | Phe |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Gly | Thr | Thr | Leu | Asn | Leu | Leu | Ser | Asn | Thr | Ile | Phe | Ser | Lys | Asp | Leu |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Thr | Asn | Pro | Phe | Ser | Asp | Ser | Ala | Lys | Glu | Phe | Lys | Glu | Leu | Val | Trp |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Asn | Ile | Met | Val | Glu | Ala | Gly | Lys | Pro | Asn | Leu | Val | Asp | Tyr | Phe | Pro |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Phe | Leu | Glu | Lys | Ile | Asp | Pro | Gln | Gly | Ile | Lys | Arg | Arg | Met | Thr | Asn |
| | 225 | | | | 230 | | | | | 235 | | | | | 240 |
| Asn | Phe | Thr | Lys | Phe | Leu | Gly | Leu | Ile | Ser | Gly | Leu | Ile | Asp | Asp | Arg |
| | | | | 245 | | | | 250 | | | | | | 255 | |
| Leu | Lys | Glu | Arg | Asn | Leu | Arg | Asp | Asn | Ala | Asn | Ile | Asp | Val | Leu | Asp |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Ala | Leu | Leu | Asn | Ile | Ser | Gln | Glu | Asn | Pro | Glu | Glu | Ile | Asp | Arg | Asn |
| | | 275 | | | | | 280 | | | | | 285 | | | |
| Gln | Ile | Glu | Gln | Leu | Cys | Leu | Asp | Leu | Phe | Ala | Ala | Gly | Thr | Asp | Thr |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Thr | Ser | Asn | Thr | Leu | Glu | Trp | Ala | Met | Ala | Glu | Leu | Leu | Gln | Asn | Pro |
| | 305 | | | | 310 | | | | | 315 | | | | | 320 |
| His | Thr | Leu | Gln | Lys | Ala | Gln | Glu | Glu | Leu | Ala | Gln | Val | Ile | Gly | Lys |
| | | | | 325 | | | | | 330 | | | | | 335 | |
| Gly | Lys | Gln | Val | Glu | Glu | Ala | Asp | Val | Gly | Arg | Leu | Pro | Tyr | Leu | Arg |
| | | | 340 | | | | | 345 | | | | | 350 | | |
| Cys | Ile | Val | Lys | Glu | Thr | Leu | Arg | Ile | His | Pro | Ala | Ala | Pro | Leu | Leu |
| | | 355 | | | | | 360 | | | | | 365 | | | |
| Ile | Pro | Arg | Lys | Val | Glu | Glu | Asp | Val | Glu | Leu | Ser | Thr | Tyr | Ile | Ile |
| | 370 | | | | | 375 | | | | | 380 | | | | |
| Pro | Lys | Asp | Ser | Gln | Val | Leu | Val | Asn | Val | Trp | Ala | Ile | Gly | Arg | Asn |
| | 385 | | | | 390 | | | | | 395 | | | | | 400 |
| Ser | Asp | Leu | Trp | Glu | Asn | Pro | Leu | Val | Phe | Lys | Pro | Glu | Arg | Phe | Trp |
| | | | | 405 | | | | | 410 | | | | | 415 | |
| Glu | Ser | Glu | Ile | Asp | Ile | Arg | Gly | Arg | Asp | Phe | Glu | Leu | Ile | Pro | Phe |
| | | | 420 | | | | | 425 | | | | | 430 | | |
| Gly | Ala | Gly | Arg | Arg | Ile | Cys | Pro | Gly | Leu | Pro | Leu | Ala | Met | Arg | Met |
| | | 435 | | | | | 440 | | | | | 445 | | | |
| Ile | Pro | Val | Ala | Leu | Gly | Ser | Leu | Leu | Asn | Ser | Phe | Asn | Trp | Lys | Leu |
| | 450 | | | | | 455 | | | | | 460 | | | | |
| Tyr | Gly | Gly | Ile | Ala | Pro | Lys | Asp | Leu | Asp | Met | Gln | Glu | Lys | Phe | Gly |
| | 465 | | | | 470 | | | | | 475 | | | | | 480 |
| Ile | Thr | Leu | Ala | Lys | Ala | Gln | Pro | Leu | Leu | Ala | Ile | Pro | Thr | Pro | Leu |
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<211> 513

<212> PRT

<213> Arabidopsis thaliana

<400> 42

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20 25 30
Leu Pro Pro Gly Pro Asn Pro Trp Pro Ile Ile Gly Asn Leu Pro His
35 40 45
Met Gly Thr Lys Pro His Arg Thr Leu Ser Ala Met Val Thr Thr Tyr
50 55 60
Gly Pro Ile Leu His Leu Arg Leu Gly Phe Val Asp Val Val Val Ala
65 70 75 80
Ala Ser Lys Ser Val Ala Glu Gln Phe Leu Lys Ile His Asp Ala Asn
85 90 95
Phe Ala Ser Arg Pro Pro Asn Ser Gly Ala Lys His Met Ala Tyr Asn
100 105 110
Tyr Gln Asp Leu Val Phe Ala Pro Tyr Gly His Arg Trp Arg Leu Leu
115 120 125
Arg Lys Ile Ser Ser Val His Leu Phe Ser Ala Lys Ala Leu Glu Asp
130 135 140
Phe Lys His Val Arg Gln Glu Glu Val Gly Thr Leu Thr Arg Glu Leu
145 150 155 160
Val Arg Val Gly Thr Lys Pro Val Asn Leu Gly Gln Leu Val Asn Met
165 170 175
Cys Val Val Asn Ala Leu Gly Arg Glu Met Ile Gly Arg Arg Leu Phe
180 185 190
Gly Ala Asp Ala Asp His Lys Ala Asp Glu Phe Arg Ser Met Val Thr
195 200 205
Glu Met Met Ala Leu Ala Gly Val Phe Asn Ile Gly Asp Phe Val Pro
210 215 220
Ser Leu Asp Trp Leu Asp Leu Gln Gly Val Ala Gly Lys Met Lys Arg
225 230 235 240
Leu His Lys Arg Phe Asp Ala Phe Leu Ser Ser Ile Leu Lys Glu His
245 250 255
Glu Met Asn Gly Gln Asp Gln Lys His Thr Asp Met Leu Ser Thr Leu
260 265 270
Ile Ser Leu Lys Gly Thr Asp Leu Asp Gly Asp Gly Gly Ser Leu Thr
275 280 285
Asp Thr Glu Ile Lys Ala Leu Leu Leu Asn Met Phe Thr Ala Gly Thr
290 295 300

Asp Thr Ser Ala Ser Thr Val Asp Trp Ala Ile Ala Glu Leu Ile Arg
305 310 315 320
His Pro Asp Ile Met Val Lys Ala Gln Glu Glu Leu Asp Ile Val Val
325 330 335

Gly Arg Asp Arg Pro Val Asn Glu Ser Asp Ile Ala Gln Leu Pro Tyr
 340 345 350

 Leu Gln Ala Val Ile Lys Glu Asn Phe Arg Leu His Pro Pro Thr Pro
 355 360 365

 Leu Ser Leu Pro His Ile Ala Ser Glu Ser Cys Glu Ile Asn Gly Tyr
 370 375 380

 His Ile Pro Lys Gly Ser Thr Leu Leu Thr Asn Ile Trp Ala Ile Ala
 385 390 395 400

 Arg Asp Pro Asp Gln Trp Ser Asp Pro Leu Ala Phe Lys Pro Glu Arg
 405 410 415

 Phe Leu Pro Gly Gly Glu Lys Ser Gly Val Asp Val Lys Gly Ser Asp
 420 425 430

 Phe Glu Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Leu
 435 440 445

 Ser Leu Gly Leu Arg Thr Ile Gln Phe Leu Thr Ala Thr Leu Val Gln
 450 455 460

 Gly Phe Asp Trp Glu Leu Ala Gly Gly Val Thr Pro Glu Lys Leu Asn
 465 470 475 480

 Met Glu Glu Ser Tyr Gly Leu Thr Leu Gln Arg Ala Val Pro Leu Val
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 Val His Pro Lys Pro Arg Leu Ala Pro Asn Val Tyr Gly Leu Gly Ser
 500 505 510

 Gly

<210> 43
 <211> 7
 <212> PRT
 <213> Arabidopsis thaliana

<400> 43
 Arg Pro Pro Asn Ser Gly Ala
 1 5

<210> 44
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 <212> PRT
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<400> 44
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Leu

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 <211> 521
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 <213> Arabidopsis thaliana

<220>
 <221> UNSURE
 <222> (8)
 <223> Xaa can be any amino acid.

<220>
 <221> UNSURE
 <222> (10)
 <223> Xaa cab be any amino acid.

<220>
 <221> UNSURE
 <222> (15)
 <223> Xaa can be any amino acid.

<220>
 <221> UNSURE
 <222> (18)..(517)
 <223> Xaa can be any amino acid. Positions 18-517
 can be 0-500 amino acids.

<400> 45
 Arg Pro Pro Asn Ser Gly Ala Xaa His Xaa Ala Tyr Asn Tyr Xaa Asp
 1 5 10 15

Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 35 40 45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 50 55 60

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 65 70 75 80

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 85 90 95

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 100 105 110

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 115 120 125

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa |
| | 130 | | | | | | 135 | | | | | 140 | | | |
| Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa |
| 145 | | | | | | 150 | | | | | 155 | | | | 160 |
| Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa |
| | | | | 165 | | | | | | 170 | | | | 175 | |
| Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa |
| | 210 | | | | | | 215 | | | | | 220 | | | |
| Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa |
| 225 | | | | | | 230 | | | | | 235 | | | | 240 |
| Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa |
| | | | | 245 | | | | | | 250 | | | | 255 | |
| Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa |
| | | | 260 | | | | | | 265 | | | | 270 | | |
| Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa |
| | | 275 | | | | | | 280 | | | | | 285 | | |
| Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa |
| | 290 | | | | | | 295 | | | | | 300 | | | |
| Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa |
| 305 | | | | | | 310 | | | | | 315 | | | | 320 |
| Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa |
| | | | | 325 | | | | | | 330 | | | | 335 | |
| Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa |
| | | | 340 | | | | | | 345 | | | | 350 | | |
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| | | 355 | | | | | | 360 | | | | | 365 | | |
| Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa |
| | 370 | | | | | | 375 | | | | | 380 | | | |
| Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa |
| 385 | | | | | | 390 | | | | | 395 | | | | 400 |
| Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa |
| | | | | 405 | | | | | | 410 | | | | 415 | |
| Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa |
| | | | 420 | | | | | | 425 | | | | 430 | | |
| Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa |
| | | 435 | | | | | | 440 | | | | | 445 | | |
| Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa |
| | 450 | | | | | | 455 | | | | | 460 | | | |

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
465 470 475 480

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
485 490 495

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
500 505 510

Xaa Xaa Xaa Xaa Xaa Gly Gly Glu Lys
515 520